

# SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Nucleotide sequences which code for the methH gene

<130> 000365 BT

<140>

10 <141>

<160> 4

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 4301

<212> DNA

<213> Corynebacterium glutamicum

20

<220>

<221> CDS

<222> (385)..(4047)

<223> methH gene

25

<400> 1

```

taagggtttt ggaggcattg gccgcgaacc catcgctggt catcccggtt ttgcgcatgc 60
cacgttcgta ttcataacca atcgcgatgc cttgagccca ccagccactg acatcaaagt 120
30 tgtccacgat gtgctttgcg atgtgggtgt gagtccaaga ggtggctttt acgtcgtcaa 180
gcaatttttag ccactcttcc cacggctttc cggtgccggt gaggatagct tcaggggaca 240
35 tgcttggtgt tgagccttgc ggagtggagt cagtcatgcg accgagacta gtggcgcttt 300
gcctgtgttg cttaggcggc gttgaaaatg aactacgaat gaaaagtctg ggaattgtct 360
aatccgtact aagctgtcta caca atg tct act tca gtt act tca cca gcc 411
40 Met Ser Thr Ser Val Thr Ser Pro Ala
      1              5

cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg ttg gca aac cat 459
His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala Leu Ala Asn His
45 10              15              20              25

gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc caa ggc ttt gac 507
Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu Gln Gly Phe Asp
      30              35              40

50 ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg tgt aat gag att 555
Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly Cys Asn Glu Ile
      45              50              55

55 ctc aac gac acc cgc cct gat gtg ttg agg cag att cac cgc gcc tac 603
Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile His Arg Ala Tyr
      60              65              70

ttt gag gcg gga gct gac ttg gtt gag acc aat act ttt ggt tgc aac 651

```

	Phe	Glu	Ala	Gly	Ala	Asp	Leu	Val	Glu	Thr	Asn	Thr	Phe	Gly	Cys	Asn	
	75						80					85					
5	ctg	ccg	aac	ttg	gcg	gat	tat	gac	atc	gct	gat	cgt	tgc	cgt	gag	ctt	699
	Leu	Pro	Asn	Leu	Ala	Asp	Tyr	Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu	
	90					95					100					105	
10	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct	gat	gag	atg	ggg	747
	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala	Asp	Glu	Met	Gly	
					110					115					120		
15	ccg	ggc	cga	aac	ggc	atg	cgg	cgt	ttc	gtg	gtt	ggg	tcc	ctg	gga	cct	795
	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly	Ser	Leu	Gly	Pro	
				125					130					135			
20	gga	acg	aag	ctt	cca	tcg	ctg	ggc	cat	gca	ccg	tat	gca	gat	ttg	cgt	843
	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr	Ala	Asp	Leu	Arg	
			140					145					150				
25	ggg	cac	tac	aag	gaa	gca	gcg	ctt	ggc	atc	atc	gac	ggg	ggg	ggc	gat	891
	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp	Gly	Gly	Gly	Asp	
		155					160					165					
30	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag	gtc	aag	gct	gcg	939
	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala	
	170					175					180					185	
35	gtt	cac	ggc	gtt	caa	gat	gcc	atg	gct	gaa	ctt	gat	aca	ttc	ttg	ccc	987
	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	
					190					195					200		
40	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	atg	ctc	atg	ggg	1035
	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly	
				205					210					215			
45	tct	gag	atc	ggg	gcc	gcg	ttg	aca	gcg	ctg	cag	cca	ctg	ggg	atc	gac	1083
	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp	
			220				225						230				
50	atg	att	ggg	ctg	aac	tgc	gcc	acc	ggc	cca	gat	gag	atg	agc	gag	cac	1131
	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu	Met	Ser	Glu	His	
		235					240					245					
55	ctg	cgt	tac	ctg	tcc	aag	cac	gcc	gat	att	cct	gtg	tcg	gtg	atg	cct	1179
	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro	
	250					255					260					265	
60	aac	gca	ggg	ctt	cct	gtc	ctg	ggg	aaa	aac	ggg	gca	gaa	tac	cca	ctt	1227
	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu	
					270				275						280		
65	gag	gct	gag	gat	ttg	gcg	cag	gcg	ctg	gct	gga	ttc	gtc	tcc	gaa	tat	1275
	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	
				285					290					295			
70	ggc	ctg	tcc	atg	gtg	ggg	ggg	tgt	tgt	ggc	acc	aca	cct	gag	cac	atc	1323
	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	
			300					305					310				
75	cgt	gcg	gtc	cgc	gat	gcg	gtg	gtt	ggg	gtt	cca	gag	cag	gaa	acc	tcc	1371
	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	

	315	320	325	
5	aca ctg acc aag atc cct gca ggc cct gtt gag cag gcc tcc cgc gag Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln Ala Ser Arg Glu 330 335 340 345	1419		
10	gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc tcg gtg cca ttg Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr Ser Val Pro Leu 350 355 360	1467		
15	tcc cag gaa acc ggc att tcc atg atc ggt gag cgc acc aac tcc aac Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg Thr Asn Ser Asn 365 370 375	1515		
20	ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc gat tgg gaa aag Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly Asp Trp Glu Lys 380 385 390	1563		
25	tgt gtg gat att gcc aag cag caa acc cgc gat ggt gca cac atg ctg Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly Ala His Met Leu 395 400 405	1611		
30	gat ctt tgt gtg gat tac gtg gga cga gac ggc acc gcc gat atg gcg Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr Ala Asp Met Ala 410 415 420 425	1659		
35	acc ttg gca gca ctt ctt gct acc agc tcc act ttg cca atc atg att Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu Pro Ile Met Ile 430 435 440	1707		
40	gac tcc acc gag cca gag gtt att cgc aca ggc ctt gag cac ttg ggt Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu Glu His Leu Gly 445 450 455	1755		
45	gga cga agc atc gtt aac tcc gtc aac ttt gaa gac ggc gat ggc cct Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp Gly Asp Gly Pro 460 465 470	1803		
50	gag tcc cgc tac cag cgc atc atg aaa ctg gta aag cag cac ggt gcg Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys Gln His Gly Ala 475 480 485	1851		
55	gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag gca cgt acc gct Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln Ala Arg Thr Ala 490 495 500 505	1899		
60	gag cac aag gtg cgc att gct aaa cga ctg att gac gat atc acc ggc Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp Asp Ile Thr Gly 510 515 520	1947		
65	agc tac ggc ctg gat atc aaa gac atc gtt gtg gac tgc ctg acc ttc Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp Cys Leu Thr Phe 525 530 535	1995		

	ccg atc tct act ggc cag gaa gaa acc agg cga gat ggc att gaa acc	2043
	Pro Ile Ser Thr Gly Gln Glu Thr Arg Arg Asp Gly Ile Glu Thr	
	540 545 550	
5	atc gaa gcc atc cgc gag ctg aag aag ctc tac cca gaa atc cac acc	2091
	Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro Glu Ile His Thr	
	555 560 565	
10	acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac cct gct gca cgc	2139
	Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn Pro Ala Ala Arg	
	570 575 580 585	
15	cag gtt ctt aac tct gtg ttc ctc aat gag tgc att gag gct ggt ctg	2187
	Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile Glu Ala Gly Leu	
	590 595 600	
20	gac tct gcg att gcg cac agc tcc aag att ttg ccg atg aac cgc att	2235
	Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro Met Asn Arg Ile	
	605 610 615	
25	gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc tat gat cgc cgc	2283
	Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val Tyr Asp Arg Arg	
	620 625 630	
30	acc gag gat tac gat ccg ctg cag gaa ttc atg cag ctg ttt gag ggc	2331
	Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln Leu Phe Glu Gly	
	635 640 645	
35	gtt tct gct gcc gat gcc aag gat gct cgc gct gaa cag ctg gcc gct	2379
	Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu Gln Leu Ala Ala	
	650 655 660 665	
40	atg cct ttg ttt gag cgt ttg gca cag cgc atc atc gac ggc gat aag	2427
	Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile Asp Gly Asp Lys	
	670 675 680	
45	aat ggc ctt gag gat gat ctg gaa gca ggc atg aag gag aag tct cct	2475
	Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys Glu Lys Ser Pro	
	685 690 695	
50	att gcg atc atc aac gag gac ctt ctc aac ggc atg aag acc gtg ggt	2523
	Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met Lys Thr Val Gly	
	700 705 710	
55	gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc gtg ctg caa tcg	2571
	Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser	
	715 720 725	
60	gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa ccg ttc atg gaa	2619
	Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu Pro Phe Met Glu	
	730 735 740 745	
65	gag gaa gca gaa gct acc gga tct gcg cag gca gag ggc aag ggc aaa	2667
	Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu Gly Lys Gly Lys	
	750 755 760	
70	atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat atc ggc aag aac	2715
	Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn	
	765 770 775	
75	ttg gtg gac atc att ttg tcc aac aac ggt tac gac gtg gtg aac ttg	2763

	Leu	Val	Asp	Ile	Ile	Leu	Ser	Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	
			780					785					790				
5	ggc	atc	aag	cag	cca	ctg	tcc	gcc	atg	ttg	gaa	gca	gcg	gaa	gaa	cac	2811
	Gly	Ile	Lys	Gln	Pro	Leu	Ser	Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	
			795				800					805					
10	aaa	gca	gac	gtc	atc	ggc	atg	tcg	gga	ctt	ctt	gtg	aag	tcc	acc	gtg	2859
	Lys	Ala	Asp	Val	Ile	Gly	Met	Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	
	810					815					820					825	
15	gtg	atg	aag	gaa	aac	ctt	gag	gag	atg	aac	aac	gcc	ggc	gca	tcc	aat	2907
	Val	Met	Lys	Glu	Asn	Leu	Glu	Glu	Met	Asn	Asn	Ala	Gly	Ala	Ser	Asn	
					830					835					840		
20	tac	cca	gtc	att	ttg	ggt	ggc	gct	gcg	ctg	acg	cgt	acc	tac	gtg	gaa	2955
	Tyr	Pro	Val	Ile	Leu	Gly	Gly	Ala	Ala	Leu	Thr	Arg	Thr	Tyr	Val	Glu	
				845				850						855			
25	aac	gat	ctc	aac	gag	gtg	tac	acc	ggt	gag	gtg	tac	tac	gcc	cgt	gat	3003
	Asn	Asp	Leu	Asn	Glu	Val	Tyr	Thr	Gly	Glu	Val	Tyr	Tyr	Ala	Arg	Asp	
			860					865					870				
30	gct	ttc	gag	ggc	ctg	cgc	ctg	atg	gat	gag	gtg	atg	gca	gaa	aag	cgt	3051
	Ala	Phe	Glu	Gly	Leu	Arg	Leu	Met	Asp	Glu	Val	Met	Ala	Glu	Lys	Arg	
		875					880					885					
35	ggt	gaa	gga	ctt	gat	ccc	aac	tca	cca	gaa	gct	att	gag	cag	gcg	aag	3099
	Gly	Glu	Gly	Leu	Asp	Pro	Asn	Ser	Pro	Glu	Ala	Ile	Glu	Gln	Ala	Lys	
	890					895					900					905	
40	aag	aag	gag	gaa	cgt	aag	gct	cgt	aat	gag	cgt	tcc	cgc	aag	att	gcc	3147
	Lys	Lys	Ala	Glu	Arg	Lys	Ala	Arg	Asn	Glu	Arg	Ser	Arg	Lys	Ile	Ala	
					910					915					920		
45	gag	gag	cgt	aaa	gct	aat	gag	gct	ccc	gtg	att	gtt	ccg	gag	cgt	tct	3195
	Ala	Glu	Arg	Lys	Ala	Asn	Ala	Ala	Pro	Val	Ile	Val	Pro	Glu	Arg	Ser	
				925				930						935			
50	gat	gtc	tcc	acc	gat	act	cca	acc	gag	gca	cca	ccg	ttc	tgg	gga	acc	3243
	Asp	Val	Ser	Thr	Asp	Thr	Pro	Thr	Ala	Ala	Pro	Pro	Phe	Trp	Gly	Thr	
				940				945					950				
55	cgc	att	gtc	aag	ggt	ctg	ccc	ttg	gag	gag	ttc	ttg	ggc	aac	ctt	gat	3291
	Arg	Ile	Val	Lys	Gly	Leu	Pro	Leu	Ala	Glu	Phe	Leu	Gly	Asn	Leu	Asp	
		955				960					965						
60	gag	cgc	gcc	ttg	ttc	atg	ggg	cag	tgg	ggt	ctg	aaa	tcc	acc	cgc	ggc	3339
	Glu	Arg	Ala	Leu	Phe	Met	Gly	Gln	Trp	Gly	Leu	Lys	Ser	Thr	Arg	Gly	
	970					975					980					985	
65	aac	gag	ggt	cca	agc	tat	gag	gat	ttg	gtg	gaa	act	gaa	ggc	cga	cca	3387
	Asn	Glu	Gly	Pro	Ser	Tyr	Glu	Asp	Leu	Val	Glu	Thr	Glu	Gly	Arg	Pro	
					990					995					1000		

cgc ctg cgc tac tgg ctg gat cgc ctg aag tct gag ggc att ttg gac 3435  
 Arg Leu Arg Tyr Trp Leu Asp Arg Leu Lys Ser Glu Gly Ile Leu Asp  
 1005 1010 1015

5 cac gtg gcc ttg gtg tat ggc tac ttc cca gcg gtc gcg gaa ggc gat 3483  
 His Val Ala Leu Val Tyr Gly Tyr Phe Pro Ala Val Ala Glu Gly Asp  
 1020 1025 1030

10 gac gtg gtg atc ttg gaa tcc ccg gat cca cac gca gcc gaa cgc atg 3531  
 Asp Val Val Ile Leu Glu Ser Pro Asp Pro His Ala Ala Glu Arg Met  
 1035 1040 1045

15 cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc ttg tgc atc gcg 3579  
 Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe Leu Cys Ile Ala  
 1050 1055 1060 1065

20 gat ttc att cgc cca cgc gag caa gct gtc aag gac ggc caa gtg gac 3627  
 Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp Gly Gln Val Asp  
 1070 1075 1080

25 gtc atg cca ttc cag ctg gtc acc atg ggt aat cct att gct gat ttc 3675  
 Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro Ile Ala Asp Phe  
 1085 1090 1095

30 gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag tac ttg gaa gtt 3723  
 Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu Tyr Leu Glu Val  
 1100 1105 1110

35 cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc gag tac tgg cac 3771  
 His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala Glu Tyr Trp His  
 1115 1120 1125

40 tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt gga tct gtc gct 3819  
 Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly Gly Ser Val Ala  
 1130 1135 1140 1145

45 gat ttt gat cca gaa gac aag acc aag ttc ttc gac ctg gat tac cgc 3867  
 Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp Leu Asp Tyr Arg  
 1150 1155 1160

50 ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct gat ctg gaa gac 3915  
 Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro Asp Leu Glu Asp  
 1165 1170 1175

55 cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt atc ggc gtg gag 3963  
 Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg Ile Gly Val Glu  
 1180 1185 1190

60 ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc aca gac gcg ttt 4011  
 Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser Thr Asp Ala Phe  
 1195 1200 1205

65 gtg ctc tac cac cca gag gca aag tac ttt aac gtc taacaccttt 4057  
 Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 1210 1215 1220

gagagggaaa actttccgc acattgcaga tcgtgccact ttaactaagg ttgacggcat 4117

60 gattaaggcg attttctggg acatggacgg cacgatggtg gactctgagc cacagtgggg 4177

cattgctacc tacgagctca gogaagccat gggccgccgc ctcaccccg agctccggga 4237

actcaccgtc ggctcgagcc tgccgcgcac catgcgctta tgcgcagagc acgcaggcat 4297

taca

4301

5

<210> 2

<211> 1221

<212> PRT

10 <213> Corynebacterium glutamicum

<400> 2

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser  
1 5 10 15

15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala  
20 25 30

20

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
50 55 60

25

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
85 90 95

30

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
100 105 110

35

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
130 135 140

40

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
165 170 175

45

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
180 185 190

50

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
195 200 205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
210 215 220

55

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
225 230 235 240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
245 250 255

60

	Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	
				260					265					270			
5	Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	
			275					280					285				
	Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	
		290					295					300					
10	Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	
	305					310					315					320	
	Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	
					325					330					335		
15	Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	
				340					345					350			
	Ala	Ser	Leu	Tyr	Thr	Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser	
20			355					360					365				
	Met	Ile	Gly	Glu	Arg	Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	
		370					375					380					
25	Ala	Met	Leu	Ser	Gly	Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	
	385					390					395					400	
	Gln	Thr	Arg	Asp	Gly	Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val	
				405						410					415		
30	Gly	Arg	Asp	Gly	Thr	Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala	
				420					425					430			
	Thr	Ser	Ser	Thr	Leu	Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val	
35			435					440					445				
	Ile	Arg	Thr	Gly	Leu	Glu	His	Leu	Gly	Gly	Arg	Ser	Ile	Val	Asn	Ser	
		450					455					460					
40	Val	Asn	Phe	Glu	Asp	Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile	
	465				470					475						480	
	Met	Lys	Leu	Val	Lys	Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile	
					485				490					495			
45	Asp	Glu	Glu	Gly	Gln	Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala	
				500					505					510			
	Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys	
50			515					520					525				
	Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu	
		530				535						540					
55	Glu	Thr	Arg	Arg	Asp	Gly	Ile	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Glu	Leu	
	545				550						555					560	
	Lys	Lys	Leu	Tyr	Pro	Glu	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile	
					565					570					575		
60																	



Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 5 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 10 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys  
 645 650 655  
 15 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu  
 660 665 670  
 20 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu  
 675 680 685  
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp  
 690 695 700  
 25 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln  
 705 710 715 720  
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala  
 725 730 735  
 30 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly  
 740 745 750  
 35 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys  
 755 760 765  
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser  
 770 775 780  
 40 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser  
 785 790 795 800  
 Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met  
 805 810 815  
 45 Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Glu Asn Leu Glu  
 820 825 830  
 50 Glu Met Asn Asn Ala Gly Ala Ser Asn Tyr Pro Val Ile Leu Gly Gly  
 835 840 845  
 Ala Ala Leu Thr Arg Thr Tyr Val Glu Asn Asp Leu Asn Glu Val Tyr  
 850 855 860

	Thr Gly Glu Val Tyr Tyr Ala Arg Asp Ala Phe Glu Gly Leu Arg Leu	865	870	875	880
5	Met Asp Glu Val Met Ala Glu Lys Arg Gly Glu Gly Leu Asp Pro Asn	885	890	895	
	Ser Pro Glu Ala Ile Glu Gln Ala Lys Lys Lys Ala Glu Arg Lys Ala	900	905	910	
10	Arg Asn Glu Arg Ser Arg Lys Ile Ala Ala Glu Arg Lys Ala Asn Ala	915	920	925	
	Ala Pro Val Ile Val Pro Glu Arg Ser Asp Val Ser Thr Asp Thr Pro	930	935	940	
15	Thr Ala Ala Pro Pro Phe Trp Gly Thr Arg Ile Val Lys Gly Leu Pro	945	950	955	960
20	Leu Ala Glu Phe Leu Gly Asn Leu Asp Glu Arg Ala Leu Phe Met Gly	965	970	975	
	Gln Trp Gly Leu Lys Ser Thr Arg Gly Asn Glu Gly Pro Ser Tyr Glu	980	985	990	
25	Asp Leu Val Glu Thr Glu Gly Arg Pro Arg Leu Arg Tyr Trp Leu Asp	995	1000	1005	
	Arg Leu Lys Ser Glu Gly Ile Leu Asp His Val Ala Leu Val Tyr Gly	1010	1015	1020	
30	Tyr Phe Pro Ala Val Ala Glu Gly Asp Asp Val Val Ile Leu Glu Ser	1025	1030	1035	1040
35	Pro Asp Pro His Ala Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln	1045	1050	1055	
	Gln Arg Gly Arg Phe Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu	1060	1065	1070	
40	Gln Ala Val Lys Asp Gly Gln Val Asp Val Met Pro Phe Gln Leu Val	1075	1080	1085	
	Thr Met Gly Asn Pro Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala	1090	1095	1100	
45	Asn Glu Tyr Arg Glu Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu	1105	1110	1115	1120
50	Thr Glu Ala Leu Ala Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu	1125	1130	1135	
	Lys Leu Asn Asp Gly Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys	1140	1145	1150	
55	Thr Lys Phe Phe Asp Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly	1155	1160	1165	
60	Tyr Gly Ser Cys Pro Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu	1170	1175	1180	

Leu Glu Pro Gly Arg Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu  
 185 1190 1195 1200

5 His Pro Glu Gln Ser Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala  
 1205 1210 1215

Lys Tyr Phe Asn Val  
 1220

10

<210> 3

<211> 52

<212> DNA

15 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer  
 meth-EVP5

20

<400> 3

gatctaagat ctaaaggagg acaaccatgt ctacttcagt tacttcacca gc 52

25

<210> 4

<211> 32

<212> DNA

<213> Artificial sequence

30

<220>

<223> Description of the artificial sequence: Primer  
 meth-EVP3

35

<400> 4

gatctagtcg acccctctca aaggtgtag ac 32